

#4



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RAW SEQUENCE LISTING

DATE: 03/25/2002

PATENT APPLICATION: US/09/996,617

TIME: 15:24:33

Input Set : A:\07334-340001.TXT

Output Set: N:\CRF3\03252002\I996617.raw

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4 <110> APPLICANT: Bertin, John
7 <120> TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
8     PROTEIN FAMILY AND USES THEREOF
11 <130> FILE REFERENCE: 07334-340001
13 <140> CURRENT APPLICATION NUMBER: 09/996,617
14 <141> CURRENT FILING DATE: 2001-11-27
16 <150> PRIOR APPLICATION NUMBER: 09/931,071
17 <151> PRIOR FILING DATE: 2001-08-15
19 <150> PRIOR APPLICATION NUMBER: 09/428,252
20 <151> PRIOR FILING DATE: 1999-10-27
22 <150> PRIOR APPLICATION NUMBER: 09/340,620
23 <151> PRIOR FILING DATE: 1999-06-28
25 <160> NUMBER OF SEQ ID NOS: 10
27 <170> SOFTWARE: FastSEQ for Windows Version 4.0
29 <210> SEQ ID NO: 1
30 <211> LENGTH: 5444
31 <212> TYPE: DNA
32 <213> ORGANISM: Homo sapiens
34 <220> FEATURE:
35 <221> NAME/KEY: CDS
36 <222> LOCATION: (523)...(4809)
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41 gcagctcaag ggttgatctc aggagtccag gacccaggag agggagaaga ctgaggaaca      180
42 cagaacagtg agcgttgccc acaccccatc tcccgctcacc acatctcccc tcaccctcac      240
43 cctccctgcc tggccctgga ccccatccca ggacctccct atcagctgac ttcttccagt      300
44 gtcttgcaag cccctctggg ctccctccctc ccctggcttt tcctaccact cccctctat      360
45 cggcgtctat ctgtagggtgc cctgggattt ataaaactgg gttccgaatg ctgaataaga      420
46 gacggtaaga gccaaggcaa aggacagcac tgttctctgc ctgcctgata ccctcaccac      480
47 ctgggaacat cccccagaca ccctottaac tccgggacag ag atg gct ggc gga      534
48                                     Met Ala Gly Gly
49                                     1
51 gcc tgg ggc cgc ctg gcc tgt tac ttg gag ttc ctg aag aag gag gag      582
52 Ala Trp Gly Arg Leu Ala Cys Tyr Leu Glu Phe Leu Lys Lys Glu Glu
53 5          10          15          20
55 ctg aag gag ttc cag ctt ctg ctc gcc aat aaa gcg cac tcc agg agc      630
56 Leu Lys Glu Phe Gln Leu Leu Leu Ala Asn Lys Ala His Ser Arg Ser
57          25          30          35
59 tct tcg ggt gag aca ccc gct cag cca gag aag acg agt ggc atg gag      678
60 Ser Ser Gly Glu Thr Pro Ala Gln Pro Glu Lys Thr Ser Gly Met Glu
61          40          45          50
63 gtg gcc tcg tac ctg gtg gct cag tat ggg gag cag cgg gcc tgg gac      726

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68	Leu	Ala	Leu	His	Thr	Trp	Glu	Gln	Met	Gly	Leu	Arg	Ser	Leu	Cys	Ala	
69			70					75					80				
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72	Gln	Ala	Gln	Glu	Gly	Ala	Gly	His	Ser	Pro	Ser	Phe	Pro	Tyr	Ser	Pro	
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75	agt	gaa	ccc	cac	ctg	ggg	tct	ccc	agc	caa	ccc	acc	tcc	acc	gca	gtg	870
76	Ser	Glu	Pro	His	Leu	Gly	Ser	Pro	Ser	Gln	Pro	Thr	Ser	Thr	Ala	Val	
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79	cta	atg	ccc	tgg	atc	cat	gaa	ttg	ccg	gcg	ggg	tgc	acc	cag	ggc	tca	918
80	Leu	Met	Pro	Trp	Ile	His	Glu	Leu	Pro	Ala	Gly	Cys	Thr	Gln	Gly	Ser	
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83	gag	aga	agg	gtt	ttg	aga	cag	ctg	cct	gac	aca	tct	gga	cgc	cgc	tgg	966
84	Glu	Arg	Arg	Val	Leu	Arg	Gln	Leu	Pro	Asp	Thr	Ser	Gly	Arg	Arg	Trp	
85				135					140					145			
87	aga	gaa	atc	tct	gcc	tca	ctc	ctc	tac	caa	gct	ctt	cca	agc	tcc	cca	1014
88	Arg	Glu	Ile	Ser	Ala	Ser	Leu	Leu	Tyr	Gln	Ala	Leu	Pro	Ser	Ser	Pro	
89			150					155					160				
91	gac	cat	gag	tct	cca	agc	cag	gag	tca	ccc	aac	gcc	ccc	aca	tcc	aca	1062
92	Asp	His	Glu	Ser	Pro	Ser	Gln	Glu	Ser	Pro	Asn	Ala	Pro	Thr	Ser	Thr	
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95	gca	gtg	ctg	ggg	agc	tgg	gga	tcc	cca	cct	cag	ccc	agc	cta	gca	ccc	1110
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97						185					190					195	
99	aga	gag	cag	gag	gct	cct	ggg	acc	caa	tgg	cct	ctg	gat	gaa	acg	tca	1158
100	Arg	Glu	Gln	Glu	Ala	Pro	Gly	Thr	Gln	Trp	Pro	Leu	Asp	Glu	Thr	Ser	
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103	gga	att	tac	tac	aca	gaa	atc	aga	gaa	aga	gag	aga	gag	aaa	tca	gag	1206
104	Gly	Ile	Tyr	Tyr	Thr	Glu	Ile	Arg	Glu	Arg	Glu	Arg	Glu	Lys	Ser	Glu	
105				215					220					225			
107	aaa	ggc	agg	ccc	cca	tgg	gca	gcg	gtg	gta	gga	acg	ccc	cca	cag	gcg	1254
108	Lys	Gly	Arg	Pro	Pro	Trp	Ala	Ala	Val	Val	Gly	Thr	Pro	Pro	Gln	Ala	
109				230				235					240				
111	cac	acc	agc	cta	cag	ccc	cac	cac	cac	cca	tgg	gag	cct	tct	gtg	aga	1302
112	His	Thr	Ser	Leu	Gln	Pro	His	His	His	Pro	Trp	Glu	Pro	Ser	Val	Arg	
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115	gag	agc	ctc	tgt	tcc	aca	tgg	ccc	tgg	aaa	aat	gag	gat	ttt	aac	caa	1350
116	Glu	Ser	Leu	Cys	Ser	Thr	Trp	Pro	Trp	Lys	Asn	Glu	Asp	Phe	Asn	Gln	
117						265					270					275	
119	aaa	ttc	aca	cag	ctg	cta	ctt	cta	caa	aga	cct	cac	ccc	aga	agc	caa	1398
120	Lys	Phe	Thr	Gln	Leu	Leu	Leu	Leu	Gln	Arg	Pro	His	Pro	Arg	Ser	Gln	
121				280					285					290			
123	gat	ccc	ctg	gtc	aag	aga	agc	tgg	cct	gat	tat	gtg	gag	gag	aat	cga	1446
124	Asp	Pro	Leu	Val	Lys	Arg	Ser	Trp	Pro	Asp	Tyr	Val	Glu	Glu	Asn	Arg	
125				295				300						305			
127	gga	cat	tta	att	gag	atc	aga	gac	tta	ttt	ggc	cca	ggc	ctg	gat	acc	1494
128	Gly	His	Leu	Ile	Glu	Ile	Arg	Asp	Leu	Phe	Gly	Pro	Gly	Leu	Asp	Thr	

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131	caa gaa cct cgc ata gtc ata ctg cag ggg gct gct gga att ggg aag	1542		
132	Gln Glu Pro Arg Ile Val Ile Leu Gln Gly Ala Ala Gly Ile Gly Lys			
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135	tca aca ctg gcc agg cag gtg aag gaa gcc tgg ggg aga ggc cag ctg	1590		
136	Ser Thr Leu Ala Arg Gln Val Lys Glu Ala Trp Gly Arg Gly Gln Leu			
137	345 350 355			
139	tat ggg gac cgc ttc cag cat gtc ttc tac ttc agc tgc aga gag ctg	1638		
140	Tyr Gly Asp Arg Phe Gln His Val Phe Tyr Phe Ser Cys Arg Glu Leu			
141	360 365 370			
143	gcc cag tcc aag gtg gtg agt ctc gct gag ctc atc gga aaa gat ggg	1686		
144	Ala Gln Ser Lys Val Val Ser Leu Ala Glu Leu Ile Gly Lys Asp Gly			
145	375 380 385			
147	aca gcc act ccg gct ccc att aga cag atc ctg tct agg cca gag cgg	1734		
148	Thr Ala Thr Pro Ala Pro Ile Arg Gln Ile Leu Ser Arg Pro Glu Arg			
149	390 395 400			
151	ctg ctc ttc atc ctc gat ggt gta gat gag cca gga tgg gtc ttg cag	1782		
152	Leu Leu Phe Ile Leu Asp Gly Val Asp Glu Pro Gly Trp Val Leu Gln			
153	405 410 415 420			
155	gag ccg agt tct gag ctc tgt ctg cac tgg agc cag cca cag ccg gcg	1830		
156	Glu Pro Ser Ser Glu Leu Cys Leu His Trp Ser Gln Pro Gln Pro Ala			
157	425 430 435			
159	gat gca ctg ctg ggc agt ttg ctg ggg aaa act ata ctt ccc gag gca	1878		
160	Asp Ala Leu Leu Gly Ser Leu Leu Gly Lys Thr Ile Leu Pro Glu Ala			
161	440 445 450			
163	tcc ttc ctg atc acg gct cgg acc aca gct ctg cag aac ctc att cct	1926		
164	Ser Phe Leu Ile Thr Ala Arg Thr Thr Ala Leu Gln Asn Leu Ile Pro			
165	455 460 465			
167	tct ttg gag cag gca cgt tgg gta gag gtc ctg ggg ttc tct gag tcc	1974		
168	Ser Leu Glu Gln Ala Arg Trp Val Glu Val Leu Gly Phe Ser Glu Ser			
169	470 475 480			
171	agc agg aag gaa tat ttc tac aga tat ttc aca gat gaa agg caa gca	2022		
172	Ser Arg Lys Glu Tyr Phe Tyr Arg Tyr Phe Thr Asp Glu Arg Gln Ala			
173	485 490 495 500			
175	att aga gcc ttt agg ttg gtc aaa tca aac aaa gag ctc tgg gcc ctg	2070		
176	Ile Arg Ala Phe Arg Leu Val Lys Ser Asn Lys Glu Leu Trp Ala Leu			
177	505 510 515			
179	tgt ctt gtg ccc tgg gtg tcc tgg ctg gcc tgc act tgc ctg atg cag	2118		
180	Cys Leu Val Pro Trp Val Ser Trp Leu Ala Cys Thr Cys Leu Met Gln			
181	520 525 530			
183	cag atg aag cgg aag gaa aaa ctc aca ctg act tcc aag acc acc aca	2166		
184	Gln Met Lys Arg Lys Glu Lys Leu Thr Leu Thr Ser Lys Thr Thr Thr			
185	535 540 545			
187	acc ctc tgt cta cat tac ctt gcc cag gct ctc caa gct cag cca ttg	2214		
188	Thr Leu Cys Leu His Tyr Leu Ala Gln Ala Leu Gln Ala Gln Pro Leu			
189	550 555 560			
191	gga ccc cag ctc aga gac ctc tgc tct ctg gct gct gag ggc atc tgg	2262		
192	Gly Pro Gln Leu Arg Asp Leu Cys Ser Leu Ala Ala Glu Gly Ile Trp			
193	565 570 575 580			

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195	caa	aaa	aag	acc	ctt	ttc	agt	cca	gat	gac	ctc	agg	aag	cat	ggg	tta	2310
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199	gat	ggg	gcc	atc	atc	tcc	acc	ttc	ttg	aag	atg	ggt	att	ctt	caa	gag	2358
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201				600					605					610			
203	cac	ccc	atc	cct	ctg	agc	tac	agc	ttc	att	cac	ctc	tgt	ttc	caa	gag	2406
204	His	Pro	Ile	Pro	Leu	Ser	Tyr	Ser	Phe	Ile	His	Leu	Cys	Phe	Gln	Glu	
205			615					620				625					
207	ttc	ttt	gca	gca	atg	tcc	tat	gtc	ttg	gag	gat	gag	aag	ggg	aga	ggt	2454
208	Phe	Phe	Ala	Ala	Met	Ser	Tyr	Val	Leu	Glu	Asp	Glu	Lys	Gly	Arg	Gly	
209		630					635					640					
211	aaa	cat	tct	aat	tgc	atc	ata	gat	ttg	gaa	aag	acg	cta	gaa	gca	tat	2502
212	Lys	His	Ser	Asn	Cys	Ile	Ile	Asp	Leu	Glu	Lys	Thr	Leu	Glu	Ala	Tyr	
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216	Gly	Ile	His	Gly	Leu	Phe	Gly	Ala	Ser	Thr	Arg	Phe	Leu	Leu	Gly		
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220	Leu	Leu	Ser	Asp	Glu	Gly	Glu	Arg	Glu	Met	Glu	Asn	Ile	Phe	His	Cys	
221			680					685				690					
223	cgg	ctg	tct	cag	ggg	agg	aac	ctg	atg	cag	tgg	gtc	ccg	tcc	ctg	cag	2646
224	Arg	Leu	Ser	Gln	Gly	Arg	Asn	Leu	Met	Gln	Trp	Val	Pro	Ser	Leu	Gln	
225			695					700				705					
227	ctg	ctg	ctg	cag	cca	cac	tct	ctg	gag	tcc	ctc	cac	tgc	ttg	tac	gag	2694
228	Leu	Leu	Leu	Gln	Pro	His	Ser	Leu	Glu	Ser	Leu	His	Cys	Leu	Tyr	Glu	
229		710					715					720					
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232	Thr	Arg	Asn	Lys	Thr	Phe	Leu	Thr	Gln	Val	Met	Ala	His	Phe	Glu	Glu	
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236	Met	Gly	Met	Cys	Val	Glu	Thr	Asp	Met	Glu	Leu	Leu	Val	Cys	Thr	Phe	
237				745					750					755			
239	tgc	att	aaa	ttc	agc	cgc	cac	gtg	aag	ctt	cag	ctg	att	gag	ggc		2838
240	Cys	Ile	Lys	Phe	Ser	Arg	His	Val	Lys	Lys	Leu	Gln	Leu	Ile	Glu	Gly	
241			760					765						770			
243	agg	cag	cac	aga	tca	aca	tgg	agc	ccc	acc	atg	gta	gtc	ctg	ttc	agg	2886
244	Arg	Gln	His	Arg	Ser	Thr	Trp	Ser	Pro	Thr	Met	Val	Val	Leu	Phe	Arg	
245			775					780				785					
247	tgg	gtc	cca	gtc	aca	gat	gcc	tat	tgg	cag	att	ctc	ttc	tcc	gtc	ctc	2934
248	Trp	Val	Pro	Val	Thr	Asp	Ala	Tyr	Trp	Gln	Ile	Leu	Phe	Ser	Val	Leu	
249		790					795					800					
251	aag	gtc	acc	aga	aac	ctg	aag	gag	ctg	gac	cta	agt	gga	aac	tcg	ctg	2982
252	Lys	Val	Thr	Arg	Asn	Leu	Lys	Glu	Leu	Asp	Leu	Ser	Gly	Asn	Ser	Leu	
253	805				810					815					820		
255	agc	cac	tct	gca	gtg	aag	agt	ctt	tgt	aag	acc	ctg	aga	cgc	cct	cgc	3030
256	Ser	His	Ser	Ala	Val	Lys	Ser	Leu	Cys	Lys	Thr	Leu	Arg	Arg	Pro	Arg	
257				825					830					835			
259	tgc	ctc	ctg	gag	acc	ctg	cgg	ttg	gct	ggc	tgt	ggc	ctc	aca	gct	gag	3078

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264	Asp	Cys	Lys	Asp	Leu	Ala	Phe	Gly	Leu	Arg	Ala	Asn	Gln	Thr	Leu	Thr	
265			855					860					865				
267	gag	ctg	gac	ctg	agc	ttc	aat	gtg	ctc	acg	gat	gct	gga	gcc	aaa	cac	3174
268	Glu	Leu	Asp	Leu	Ser	Phe	Asn	Val	Leu	Thr	Asp	Ala	Gly	Ala	Lys	His	
269			870				875					880					
271	ctt	tgc	cag	aga	ctg	aga	cag	ccg	agc	tgc	aag	cta	cag	cga	ctg	cag	3222
272	Leu	Cys	Gln	Arg	Leu	Arg	Gln	Pro	Ser	Cys	Lys	Leu	Gln	Arg	Leu	Gln	
273	885						890					895				900	
275	ctg	gtc	agc	tgt	ggc	ctc	acg	tct	gac	tgc	tgc	cag	gac	ctg	gcc	tct	3270
276	Leu	Val	Ser	Cys	Gly	Leu	Thr	Ser	Asp	Cys	Cys	Gln	Asp	Leu	Ala	Ser	
277				905					910				915				
279	gtg	ctt	agt	gcc	agc	ccc	agc	ctg	aag	gag	cta	gac	ctg	cag	cag	aac	3318
280	Val	Leu	Ser	Ala	Ser	Pro	Ser	Leu	Lys	Glu	Leu	Asp	Leu	Gln	Gln	Asn	
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283	aac	ctg	gat	gac	gtt	ggc	gtg	cga	ctg	ctc	tgt	gag	ggg	ctc	agg	cat	3366
284	Asn	Leu	Asp	Val	Gly	Val	Arg	Leu	Leu	Cys	Glu	Gly	Leu	Arg	His		
285			935				940					945					
287	cct	gcc	tgc	aaa	ctc	ata	cgc	ctg	ggg	ctg	gac	cag	aca	act	ctg	agt	3414
288	Pro	Ala	Cys	Lys	Leu	Ile	Arg	Leu	Gly	Leu	Asp	Gln	Thr	Thr	Leu	Ser	
289			950				955					960					
291	gat	gag	atg	agg	cag	gaa	ctg	agg	gcc	ctg	gag	cag	gag	aaa	cct	cag	3462
292	Asp	Glu	Met	Arg	Gln	Glu	Leu	Arg	Ala	Leu	Glu	Gln	Glu	Lys	Pro	Gln	
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295	ctg	ctc	atc	ttc	agc	aga	cgg	aaa	cca	agt	gtg	atg	acc	cct	act	gag	3510
296	Leu	Leu	Ile	Phe	Ser	Arg	Arg	Lys	Pro	Ser	Val	Met	Thr	Pro	Thr	Glu	
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301				1000					1005				1010				
303	cag	aga	ctc	gga	tca	gag	agg	gcg	gct	tcc	cat	gtt	gct	cag	gct	aat	3606
304	Gln	Arg	Leu	Gly	Ser	Glu	Arg	Ala	Ala	Ser	His	Val	Ala	Gln	Ala	Asn	
305			1015					1020					1025				
307	ctc	aaa	ctc	ctg	gac	gtg	agc	aag	atc	ttc	cca	att	gct	gag	att	gca	3654
308	Leu	Lys	Leu	Leu	Asp	Val	Ser	Lys	Ile	Phe	Pro	Ile	Ala	Glu	Ile	Ala	
309			1030				1035					1040					
311	gag	gaa	agc	tcc	cca	gag	gta	gta	ccg	gtg	gaa	ctc	ttg	tgc	gtg	cct	3702
312	Glu	Glu	Ser	Ser	Pro	Glu	Val	Val	Pro	Val	Glu	Leu	Leu	Cys	Val	Pro	
313	1045					1050					1055					1060	
315	tct	cct	gcc	tct	caa	ggg	gac	ctg	cat	acg	aag	cct	ttg	ggg	act	gac	3750
316	Ser	Pro	Ala	Ser	Gln	Gly	Asp	Leu	His	Thr	Lys	Pro	Leu	Gly	Thr	Asp	
317				1065					1070				1075				
319	gat	gac	ttc	tgg	ggc	ccc	acg	ggg	cct	gtg	gct	act	gag	gta	gtt	gac	3798
320	Asp	Asp	Phe	Trp	Gly	Pro	Thr	Gly	Pro	Val	Ala	Thr	Glu	Val	Val	Asp	
321				1080					1085				1090				
323	aaa	gaa	aag	aac	ttg	tac	cga	gtt	cac	ttc	cct	gta	gct	ggc	tcc	tac	3846
324	Lys	Glu	Lys	Asn	Leu	Tyr	Arg	Val	His	Phe	Pro	Val	Ala	Gly	Ser	Tyr	

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